

JAN 07 2002

# SEQUENCE LISTING

<110> NAKANE et al.

<120> FARNESYL DIPHOSPHATE SYNTHASE

<130> 77670-593

<140> 09/902,651

<141> 2001-07-12

<150> 08/898,560

<151> 1997-07-22

<150> JP8-213211

<151> 1996-07-24

<160> 14

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<211> 330

<212> PRT

<213> Sulfolobus acidocaldarius

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Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu  
35 40 45  
Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala  
50 55 60  
Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val  
65 70 75 80  
His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr  
85 90 95  
Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu  
100 105 110  
Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu  
115 120 125  
Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile  
130 135 140  
Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg  
145 150 155 160  
Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr  
165 170 175  
Ala Ala Leu Phe Ser Ala Ser Ser Ser Ile Gly Ala Leu Ile Ala Gly  
180 185 190  
Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu  
195 200 205  
Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp  
210 215 220  
Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys  
225 230 235 240  
Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu  
245 250 255  
Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu  
260 265 270  
Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr

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275	280	285
Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu		
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Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr		
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Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys		320
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gac att att aag agc tat ata tct gga gat gtt cct aaa cta tat gaa	96
Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu	
20 25 30	
gcc tca tat cat ttg ttt aca tct gga ggt aag agg tta aga cca tta	144
Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu	
35 40 45	
atc tta act ata tca tca gat tta ttc gga gga cag aga gaa aga gct	192
Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala	
50 55 60	
tat tat gca ggt gca gct att gaa gtt ctt cat act ttt acg ctt gtg	240
Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val	
65 70 75 80	
cat gat gat att atg gat caa gat aat atc aga aga ggg tta ccc aca	288
His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr	
85 90 95	
gtc cac gtg aaa tac ggc tta ccc tta gca ata tta gct ggg gat tta	336
Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu	
100 105 110	
cta cat gca aag gct ttt cag ctc tta acc cag gct ctt aga ggt ttg	384
Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu	
115 120 125	
cca agt gaa acc ata att aag gct ttc gat att ttc act cgt tca ata	432
Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile	
130 135 140	
ata att ata tcc gaa gga cag gca gta gat atg gaa ttt gag gac aga	480
Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg	
145 150 155 160	
att gat ata aag gag cag gaa tac ctt gac atg atc tca cgt aag aca	528
Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr	
165 170 175	

gct gca tta ttc tcg gca tcc tca agt ata ggc gca ctt att gct ggt	576
Ala Ala Leu Phe Ser Ala Ser Ser Ile Gly Ala Leu Ile Ala Gly	
180 185 190	
gct aat gat aat gat gta aga ctg atg tct gat ttc ggt acg aat cta	624
Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu	
195 200 205	
ggg att gca ttt cag att gtt gac gat atc tta ggt cta aca gca gac	672
Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp	
210 215 220	
gaa aag gaa ctt gga aag cct gtt ttt agt gat att agg gag ggt aaa	720
Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys	
225 230 235 240	
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Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu	
245 250 255	
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Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu	
260 265 270	
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Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr	
275 280 285	
gca tac aat tta gca gag aaa tat tat aaa aat gct ata gac tct tta	912
Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu	
290 295 300	
aat caa gtc tcc tct aag agt gat ata cct gga aag gct tta aaa tat	960
Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr	
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Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys *	
325 330	

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